OIPE

RAW SEQUENCE LISTING   DATE: 11/13/2001
PATENT APPLICATION: US/09/841,963   TIME: 15:37:56

Input Set : N:\Crf3\RULE60\09841963.txt
Output Set: N:\CRF3\11132001\I841963.raw

ENTERED

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 4 <110> APPLICANT: MUSC FOUNDATION FOR RESEARCH DEVELOPMENT
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSIS AND TREATMENT
 7       OF CANCER BASED ON THE TRANSCRIPTION FACTOR ETS2
 9 <130> FILE REFERENCE: 9175-006-228
11 <140> CURRENT APPLICATION NUMBER: 09/841,963
12 <141> CURRENT FILING DATE: 2001-04-25
14 <150> PRIOR APPLICATION NUMBER: 99/27805
15 <151> PRIOR FILING DATE: 1999-11-23
17 <160> NUMBER OF SEQ ID NOS: 34
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2269
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (292)...(1698)
30 <400> SEQUENCE: 1
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32 ctcccgctcc tgaagagcgc gccgcgtggg ggacggcccg gttacttcct ccagagactg     120
33 acgagtgcgg tgtcgctcca gctcagagct cccggagccg cccggccagc gtccggcctc     180
34 cctgatcgtc tctggccggc gccctcgccc tcgccccggc cgcaccgagc agccgcgggc     240
35 gccgagcagc caccgtcccg accaagcgcc ggccctgccc gcagcggcag g atg aat     297
36                                                           Met Asn
37                                                             1
39 gat ttc gga atc aag aat atg gac cag gta gcc cct gtg gct aac agt     345
40 Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala Asn Ser
41         5                  10                  15
43 tac aga ggg aca ctc aag cgc cag cca gcc ttt gac acc ttt gat ggg     393
44 Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe Asp Gly
45      20                  25                  30
47 tcc ctg ttt gct gtt ttt cct tct cta aat gaa gag caa aca ctg caa     441
48 Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr Leu Gln
49   35                  40                  45                  50
51 gaa gtg cca aca ggc ttg gat tcc att tct cat gac tcc gcc aac tgt     489
52 Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala Asn Cys
53                  55                  60                  65
55 gaa ttg cct ttg tta acc ccg tgc agc aag gct gtg atg agt caa gcc     537
56 Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser Gln Ala
57              70                  75                  80
59 tta aaa gct acc ttc agt ggc ttc aaa aag gaa cag cgg cgc ctg ggc     585
60 Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg Leu Gly
61          85                  90                  95
63 att cca aag aac ccc tgg ctg tgg agt gag caa cag gta tgc cag tgg     633
64 Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys Gln Trp
65     100                 105                 110
67 ctt ctc tgg gcc acc aat gag ttc agt ctg gtg aac gtg aat ctg cag     681
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 68  Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn Leu Gln
 69  115             120             125             130
 71  agg ttc ggc atg aat ggc cag atg ctg tgt aac ctt ggc aag gaa cgc      729
 72  Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys Glu Arg
 73              135             140             145
 75  ttt ctg gag ctg gca cct gac ttt gtg ggt gac att ctc tgg gaa cat      777
 76  Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp Glu His
 77              150             155             160
 79  ctg gag caa atg atc aaa gaa aac caa gaa aag aca gaa gat caa tat      825
 80  Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp Gln Tyr
 81          165             170             175
 83  gaa gaa aat tca cac ctc acc tcc gtt cct cat tgg att aac agc aat      873
 84  Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn Ser Asn
 85      180             185             190
 87  aca tta ggt ttt ggc aca gag cag gcg ccc tat gga atg cag aca cag      921
 88  Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln Thr Gln
 89  195             200             205             210
 91  aat tac ccc aaa ggc ggc ctc ctg gac agc atg tgt ccg gcc tcc aca      969
 92  Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala Ser Thr
 93              215             220             225
 95  ccc agc gta ctc agc tct gag cag gag ttt cag atg ttc ccc aag tct     1017
 96  Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro Lys Ser
 97              230             235             240
 99  cgg ctc agc tcc gtc agc gtc acc tac tgc tct gtc agt cag gac ttc     1065
100  Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln Asp Phe
101          245             250             255
103  cca ggc agc aac ttg aat ttg ctc acc aac aat tct ggg act ccc aaa     1113
104  Pro Gly Ser Asn Leu Asn Leu Leu Thr Asn Asn Ser Gly Thr Pro Lys
105      260             265             270
107  gac cac gac tcc cct gag aac ggt gcg gac agc ttc gag agc tca gac     1161
108  Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser Ser Asp
109  275             280             285             290
111  tcc ctc ctc cag tcc tgg aac agc cag tcg tcc ttg ctg gat gtg caa     1209
112  Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp Val Gln
113              295             300             305
115  cgg gtt cct tcc ttc gag agc ttc gaa gat gac tgc agc cag tct ctc     1257
116  Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln Ser Leu
117              310             315             320
119  tgc ctc aat aag cca acc atg tct ttc aag gat tac atc caa gag agg     1305
120  Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln Glu Arg
121          325             330             335
123  agt gac cca gtg gag caa ggc aaa cca gtt ata cct gca gct gtg ctg     1353
124  Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala Val Leu
125          340             345             350
127  gcc ggc ttc aca gga agt gga cct att cag ctg tgg cag ttt ctc ctg     1401
128  Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu
129  355             360             365             370
131  gag ctg cta tca gac aaa tcc tgc cag tca ttc atc agc tgg act gga     1449
132  Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly
```

```
133                   375             380               385
135 gac gga tgg gag ttt aag ctc gcc gac ccc gat gag gtg gcc cgc cgg   1497
136 Asp Gly Trp Glu Phe Lys Leu Ala Asp Pro Asp Glu Val Ala Arg Arg
137               390             395               400
139 tgg gga aag agg aaa aat aag ccc aag atg aac tac gag aag ctg agc   1545
140 Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser
141           405             410               415
143 cgg ggc tta cgc tac tat tac gac aag aac atc atc cac aag acg tcg   1593
144 Arg Gly Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ser
145       420             425             430
147 ggg aag cgc tac gtg tac cgc ttc gtg tgc gac ctc cag aac ttg ctg   1641
148 Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn Leu Leu
149 435             440             445               450
151 ggg ttc acg ccc gag gaa ctg cac gcc atc ctg ggc gtc cag ccc gac   1689
152 Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln Pro Asp
153               455             460               465
155 acg gag gac tgaggtcgcc gggaccaccc tgagccggcc ccaggctcgt           1738
156 Thr Glu Asp
159 ggactgagtg ggaagcccat cctgaccagc tgcctccgag gacccaggaa aggcaggatt   1798
160 gaaaatgtcc aggaaagtgg ccaagaagca gtggccttat tgcatcccaa accacgcctc   1858
161 ttgaccaggc tgcctccctt gtggcagcaa cggcacagct aattctactc acagtgcttt   1918
162 taagtgaaaa tggtcgagaa agaggcaccg ggaagccgtc ctggcgcctg gcagtccgtg   1978
163 ggacgggatg gttctggctg tttgagattc tcaaaggagc gagcatgtcg tggacacaca   2038
164 cagactattt ttagattttc ttttgccttt tgcaaccagg aacagcaaat gcaaaaactc   2098
165 tttgagaggg taggagggtg ggaaggaaac aaccatgtca tttcagaagt tagtttgtat   2158
166 atattataat aatcttataa ttgttctcag aatcccttaa cagttgtatt taacagaaat   2218
167 tgtatattgt aatttaaaat aattatataa ctgtatttga aataagaatt c            2269
169 <210> SEQ ID NO: 2
170 <211> LENGTH: 469
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 2
175 Met Asn Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala
176  1               5                  10                  15
177 Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe
178               20                  25                  30
179 Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr
180           35                  40                  45
181 Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala
182       50                  55                  60
183 Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser
184 65                  70                  75                  80
185 Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg
186               85                  90                  95
187 Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys
188               100                 105                 110
189 Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn
190       115                 120                 125
191 Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys
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                                  135                    140
192        130          Phe Asp Phe Val Gly Asp Ile Leu Trp
193  Glu Arg Phe Leu Glu Leu Ala Pro                          160
194  145                150           155 Gln Glu Lys Thr Glu Asp
195  Glu His Leu Glu Gln Met Ile Lys Glu Asn
196  Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn
197            180          185                 190 Gly Met Gln
198  Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr
199       195           200                    205 Met Cys Pro Ala
200  Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser
201       210           215                 220 Gln Met Phe Pro
202  Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe            240
203  225                230              235 Tyr Cys Ser Val Ser Gln
204  Lys Ser Arg Leu Ser Ser Val Ser Val Thr                   255
205            245              250 Thr Asn Asn Ser Gly Thr
206  Asp Phe Pro Gly Ser Asn Leu Asn Leu Leu                   270
207       260              265 Ala Asp Ser Phe Glu Ser
208  Pro Lys Asp His Asp Ser Pro Glu Asn Gly                   285
209       275              280 Ser Ser Ser Leu Leu Asp
210  Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln              300
211       290              295 Asp Asp Cys Ser Gln
212  Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu              320
213  305                310              315 Phe Lys Asp Tyr Ile Gln
214  Ser Leu Cys Leu Asn Lys Pro Thr Met Ser                  335
215            325              330 Pro Val Ile Pro Ala Ala
216  Glu Arg Ser Asp Pro Val Glu Gln Gly Lys                  350
217       340              345 Ile Gln Leu Trp Gln Phe
218  Val Leu Ala Gly Phe Thr Gly Ser Gly Pro              365
219       355              360 Ser Phe Ile Ser Trp
220  Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln             380
221       370              375 Pro Asp Glu Val Ala
222  Thr Gly Asp Gly Trp Glu Phe Lys Leu Ala Asp             400
223  385                390              395 Met Asn Tyr Glu Lys
224  Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro                  415
225            405              410 Asp Lys Asn Ile Ile His Lys
226  Leu Ser Arg Gly Leu Arg Tyr Tyr Tyr                      430
227       420              425 Phe Val Cys Asp Leu Gln Asn
228  Thr Ser Gly Lys Arg Tyr Val Tyr Arg                      445
229       435              440 Ile Leu Gly Val Gln
230  Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala              460
231       450              455
232  Pro Asp Thr Glu Asp
233       465
234  236 <210> SEQ ID NO: 3
237  <211> LENGTH: 84
238  <212> TYPE: PRT
239  <213> ORGANISM: Homo sapiens
241  <400> SEQUENCE: 3
242  Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Thr Asp
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```
243   1                  5                  10                 15
244   Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly Asp Gly Trp Glu Phe
245                  20                 25                 30
246   Lys Leu Ser Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Lys Arg Lys
247              35                 40                 45
248   Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser Arg Gly Leu Arg Tyr
249          50                 55                 60
250   Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ala Gly Lys Arg Tyr Val
251   65                 70                 75                 80
252   Tyr Arg Phe Val
255  <210> SEQ ID NO: 4
256  <211> LENGTH: 84
257  <212> TYPE: PRT
258  <213> ORGANISM: Mus musculus
260  <400> SEQUENCE: 4
261   Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Thr Asp
262   1                  5                  10                 15
263   Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly Asp Gly Trp Glu Phe
264                  20                 25                 30
265   Lys Leu Ser Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Lys Arg Lys
266              35                 40                 45
267   Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser Arg Gly Leu Arg Tyr
268          50                 55                 60
269   Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ala Gly Lys Arg Tyr Val
270   65                 70                 75                 80
271   Tyr Arg Phe Val
274  <210> SEQ ID NO: 5
275  <211> LENGTH: 84
276  <212> TYPE: PRT
277  <213> ORGANISM: Gallus gallus
279  <400> SEQUENCE: 5
280   Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Thr Asp
281   1                  5                  10                 15
282   Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly Asp Gly Trp Glu Phe
283                  20                 25                 30
284   Lys Leu Ser Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Lys Arg Lys
285              35                 40                 45
286   Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser Arg Gly Leu Arg Tyr
287          50                 55                 60
288   Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ala Gly Lys Arg Tyr Val
289   65                 70                 75                 80
290   Tyr Arg Phe Val
293  <210> SEQ ID NO: 6
294  <211> LENGTH: 84
295  <212> TYPE: PRT
296  <213> ORGANISM: Xenopus laevis
298  <400> SEQUENCE: 6
299   Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Thr Asp
300   1                  5                  10                 15
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/841,963

DATE: 11/13/2001
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Input Set : N:\Crf3\RULE60\09841963.txt
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